

-continued

<400> SEQUENCE: 16

gtgaaaaggaa agagagaaca aacacccggg agagacatca accaaaatcc agtccccagt	60
tttacacgcgt gaaagcactg ggatgcgggt cgtaaacatt ttgtgggctt ggccggagact	120
attacgaccc aaataaatgc actgtgtac gtgttcacag ggctccgggg cctttcgaaa	180
ggttctctgt ttgttttg	199

<210> SEQ ID NO 17

<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 17

gtgaaaaggaa agagagaata aatatt	26
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<210> SEQ ID NO 18

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 18

caaaaacaaa caaaaacact ttc	23
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<210> SEQ ID NO 19

<211> LENGTH: 199
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Sequence of the locus specific for buccal epithelial cells after bisulfite treatment assuming 100% unmethylation of all CpG sites

<400> SEQUENCE: 19

gtgaaaaggaa agagagaata aatatttggg agagatatta attaaaattt agtttttagt	60
tttatagtgt gaaagtattt ggatgtgggt tgtaaatatt ttgtgggctt ggtggagatt	120
attatgattt aaataaatgt attgtgtatg gtgttataag ggaaaaaaa tttttttttt gaaa	180
ggttttttgt ttgttttg	199

<210> SEQ ID NO 20

<211> LENGTH: 199
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

gtgaaaaggaa agagagaaca aacacccggg agagacatca accaaaatcc agtccccagt	60
tttacacgcgt gaaagcactg ggatgcgggt cgtaaacatt ttgtgggctt ggccggagact	120
attacgaccc aaataaatgc actgtgtac gtgttcacag ggctccgggg cctttcgaaa	180
ggttctctgt ttgttttg	199

We claim:

1. A method for identifying a sample as containing or not containing a blood cell, the method comprising the steps of:

(a) determining the level of methylation at the genetic locus of SEQ ID NO: 11 in:

- i) a genomic DNA isolated from the sample, and
- ii) optionally, a control genomic DNA;

60

(b) optionally, obtaining one or more reference values corresponding to the level of methylation at the genetic locus of SEQ ID NO: 11; and

(c) identifying the sample as containing, or not containing, the blood cell based on the level of methylation at the genetic locus of SEQ ID NO: 11 in the genomic DNA isolated from the sample,

65